PENDING CLAIMS

Clean Versions of Pending Claims under 37 C.F.R. 1.121(c)(3)

1. An isolated nucleic acid molecule comprising a nucleotide sequence:

(a) as set forth in SEQ ID NO: 1;

(b) encoding a polypeptide as set forth in SEQ ID NO: 2;

(c) that hybridizes under at least moderately stringent conditions to the complement of the nucleotide sequence of either (a) or (b); or

(d) complementary to the nucleotide sequence of any of (a) - (c).

2. An isolated nucleic acid molecule comprising:

(a) a region of the nucleotide sequence of SEQ ID NO: 1 encoding a polypeptide fragment of at least 25 amino acid residues;

(b) a region of the nucleotide sequence of SEQ ID NO: 1 comprising a fragment of at least 16 nucleotides;

(c) a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of the nucleotide sequence of either (a) or (b); or

(d) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - (c).

3. An isolated nucleic acid molecule comprising:

(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 70 percent identical to the polypeptide set forth in SEQ ID NO: 2;

(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and or N- terminal truncation, wherein the encoded polypeptide comprises at least 25 amino acid residues;

(c) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at

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terminal truncation, wherein the encoded polypeptide is at least 70 percent identical to the polypeptide set forth in SEQ ID NO: 2 and comprises at least 25 amino acid residues;

(d) a region of the nucleotide sequence of any of (a) - (c) comprising a fragment of at least 16 nucleotides;

(e) a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of the nucleotide sequence of any of (a) - (d); or

(f) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - (e).

4. A vector comprising the nucleic acid molecule of any of Claims 1, 2, or 3.

5. A host cell comprising the vector of Claim 4.

6. The host cell of Claim 5 that is a eukaryotic cell.

7. The host cell of Claim 5 that is a prokaryotic cell.

8. A process of producing an IL-1ra-L polypeptide comprising culturing the host cell of Claim 5 under suitable conditions to express the polypeptide, and optionally isolating the polypeptide from the culture.

10. The process of Claim 8, wherein the nucleic acid molecule comprises promoter DNA other than native IL-1ra-L promoter DNA operatively linked to a nucleic acid molecule encoding an IL-1ra-L polypeptide.

11. The isolated nucleic acid molecule according to Claim 2, wherein the percent identity is determined using a computer program that is GAP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, or the Smith-Waterman algorithm.

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42. A composition comprising a nucleic acid molecule of any of Claims 1, 2, or 3 and a pharmaceutically acceptable formulation agent.

43. The composition of Claim 42, wherein said nucleic acid molecule is contained in a viral vector.

44. A viral vector comprising a nucleic acid molecule of any of Claims 1, 2, or 3.

45. A nucleic acid molecule encoding a fusion polypeptide comprising the nucleic acid molecule of any of Claims 1, 2, or 3 fused to DNA encoding a heterologous amino acid sequence.

46. The nucleic acid molecule of Claim 45, wherein the DNA encoding the heterologous amino acid sequence encodes an IgG constant domain or biologically active fragment thereof.

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